mutated to be substantially reduced in the ability to add one or more non-templated nucleotides to the 3′ terminus of a DNA molecule; amplifying said polymorphic DNA fragment within said sample; and analyzing said amplified polymorphic DNA fragment.

Claim 2 (Previously presented): A method of producing amplified copies of a polymorphic DNA fragment which comprise substantially no non-templated 3′ terminal nucleotides, said method comprising contacting a DNA sample with one or more DNA polymerases, wherein said DNA polymerases are mutated to be substantially reduced in the ability to add one or more non-templated nucleotides to the 3′ terminus of a DNA molecule; and amplifying said polymorphic DNA fragment within said DNA sample.

Claim 3 and Claim 4 (Previously cancelled).

Claim 5 (Original): The method of claim 1, wherein said polymorphic DNA fragment is selected from the group of polymorphic DNA fragments comprising a minisatellite DNA fragment, a microsatellite DNA fragment and a STR DNA fragment.

Claim 6 (Original): The method of claim 1, wherein said polymerases are thermostable DNA polymerases.

Claim 7 (Previously presented): The method of claim 6, wherein said thermostable DNA polymerases are *Thermotoga* DNA polymerases or mutants thereof.

Claim 8 (Original): The method of claim 7, wherein said DNA polymerase is a *Tne* or *Tma* DNA polymerase.

Claim 9 (Original): The method of claim 1, wherein said DNA polymerases are substantially reduced in 3′-5′exonuclease activity.

Claim 10 (Original): The method of claim 1, wherein said DNA polymerases are substantially reduced in 5′-3′ exonuclease activity.

Claim 11 (Original): The method of claim 9, wherein said DNA polymerases are substantially reduced in 5′-3′ exonuclease activity.

Claim 12 (Original): The method of claim 1, wherein said DNA polymerases contain one or more modifications or mutations which reduce the ability of the polymerase to add one or more non-templated 3′ nucleotides to a synthesized nucleic acid molecule.

Claim 13 (Original): The method of claim 12, wherein said DNA polymerases are substantially reduced in at least one activity selected from the group consisting of:

(a) 3′-5′ exonuclease activity; and

(b) 5′-3′ exonuclease activity.

Claim 14 (Original): The method of claim 13, wherein said polymerases have substantially reduced 3′-5′ exonuclease and 5′-3′ exonuclease activity.

Claim 15 (Original): The method of claim 13, wherein said polymerase is substantially reduced in 3′-5′ exonuclease activity.

Claim 16 (Original): The method of claim 12, wherein said polymerases comprise one or more mutations or modifications in the O-helix of said polymerase.

Claim 17 (Original): The method of claim 16, wherein said O-helix is defined as RXXXKXXXFXXXYX (SEQ ID NO:11), wherein X is any amino acid.

Claim 18 (Original): The method of claim 17, wherein said mutation or modification is at position R (Arg) and/or F (Phe) and/or K (Lys) of said O-helix or combinations thereof.

Claim 19 (Original): The method of claim 1, wherein said polymerase is selected from the group consisting of:

Tne N'Δ219, D323A;

Tne N'Δ283, D323A;

Tne N'Δ284, D323A;

Tne N'Δ193, D323A;

Tne D137A, D323A;

Tne D8A, D323A;

Tne G195D, D323A;

Tne G37D, D323A;

Tne N'Δ283;

Tne D137A, D323A, R722K;

Tne D137A, D323A, R722Y;

Tne D137A, D323A, R722L;

Tne D137A, D323A, R722H;

Tne D137A, D323A, R722Q;

Tne D137A, D323A, F730Y;

Tne D137A, D323A, K726R;

Tne D137A, D323A, K726H;

Tne D137A, D323A, R722K, F730Y;

Tne D137A, D323A, R722K, K726R;

Tne D137A, D323A, R722K, K726H;

Tne D137A, D323A, R722H, F730Y;

Tne D137A, D323A, R722H, K726R;

Tne D137A, D323A, R722H, K726H;

Tne D137A, D323A, R722Q, F730Y;

Tne D137A, D323A, R722Q, K726R;

Tne D137A, D323A, R722Q, K726H;

Tne D137A, D323A, R722N, F730Y;

Tne D137A, D323A, R722N, K726R;

Tne D137A, D323A, R722N, K726H;

Tne D137A, D323A, F730S;

Tne N'Δ283, D323A, R722K/H/Q/N/Y/L;

Tne N'Δ219, D323A, R722K;

Tne N'Δ219, D323A, F730Y;

Tne N'Δ219, D323A, K726R;

Tne N'Δ219, D323A, K726H;

Tne D137A, D323A, F730S, R722K/Y/Q/N/H/L, K726R/H;

Tne D137A, D323A, F730T, R722K/Y/Q/N/H/L, K726R/H;

Tne D137A, D323A, F730T;

Tne F730S;

Tne F730A;

Tne K726R;

Tne K726H; and

Tne D137A, D323A, R722N.

Claim 20 (Original): The method of claim 16, wherein said mutation or modification is an amino acid substitution at position R and/or F and/or K of said O-helix or combinations thereof.

Claim 21 (Previously presented): A method of determining the relationship between a first individual and a second individual, said method comprising comparing a population of amplified DNA molecules in a sample of DNA from said first individual to that of said second individual, wherein said DNA sample of said first and second individuals are analyzed according to the method of claim 1.

Claim 22 (Original): The method of claim 21, wherein said sample of DNA from said first individual is a known sample and said sample of DNA from said second individual is an unknown sample.

Claim 23 (Previously presented): A kit comprising one or more DNA polymerases, wherein said DNA polymerases are mutated to be substantially reduced in the ability to add one or more non-templated nucleotides to the 3′ terminus of a DNA molecule.

Claim 24 (Original): The kit of claim 23, said kit further comprising one or more components selected from the group consisting of one or more DNA primers, one or more deoxynucleoside triphosphates, and a buffer suitable for use in the identification, analysis or typing of a polymorphic DNA fragment.

Claim 25 (Original): The kit of claim 23, wherein said polymerases are thermostable DNA polymerases.

Claim 26 (Original): The kit of claim 25, wherein thermostable DNA polymerases are *Thermotoga* DNA polymerases.

Claim 27 (Original): The kit of claim 23, wherein said DNA polymerase is substantially reduced in 3′-5′ exonuclease activity.

Claim 28 (Original): The kit of claim 23, wherein said DNA polymerase is substantially reduced in 5′-3′ exonuclease activity.

Claim 29 (Original): The kit of claim 23, wherein said DNA polymerases comprise one or more modifications or mutations which reduce the ability of the polymerase to add one or more non-templated 3′ nucleotides to a synthesized nucleic acid molecule.

Claim 30 (Original): The kit of claim 29, wherein said polymerases comprise one or more mutations in the O-helix of said polymerase.

Claim 31 (Original): The kit of claim 30, wherein said O-helix is defined as RXXXKXXXFXXXYX (SEQ ID NO:11), wherein X is any amino acid.

Claim 32 (Original): The kit of claim 31, wherein said mutation or modification is at position R (Arg) and/or F (Phe) and/or K (Lys) of said O-helix or combinations thereof.

Claim 33 (Original): The method of claim 31, wherein said mutation or modification is an amino acid substitution at position R and/or F and/or K of said O-helix or combinations thereof.

Claims 34-65 (Previously cancelled).

Claim 66 (Currently amended): A method for amplifying a double stranded DNA molecule, comprising:

(a) providing a first and second primer, wherein said first primer is complementary to a sequence at or near the ~~3'-termini~~ 3'-terminus of the first strand of said DNA molecule and said second primer is complementary to a sequence at or near the ~~3'-termini~~ 3'-terminus of the second strand of said DNA molecule;

(b) hybridizing said first primer to said first strand and said second primer to said second strand in the presence of the one or more DNA polymerases which have been mutated to reduce, substantially reduce or eliminate the ability of the polymerases to add non-templated 3' nucleotides to a synthesized nucleic acid molecule under conditions such that a third DNA molecule complementary to said first strand and a fourth DNA molecule complementary to said second strand are synthesized;

(c) denaturing said first and third ~~strand~~ strands, and said second and fourth strands; and

(d) repeating steps (a) to (c) one or more times.

Claim 67 and Claim 68 (Previously cancelled).

Claim 69 (Previously presented): The method of any one of claims 1, 2 and 66, wherein said one or more DNA polymerases produce less than about 5% of amplification products containing one or more non-templated nucleotides at their 3′ termini.

Claim 70 (Previously presented): The method of any one of claims 1, 2 and 66, wherein said one or more DNA polymerases produce less than about 1% of amplification products containing one or more non-templated nucleotides at their 3′ termini.

Claim 71 (Previously presented): The kit of claim 23, wherein siad one or more DNA polymerases produce less than about 5% of amplification products containing one or more non-templated nucleotides at their 3′ termini.

Claim 72 (Previously presented): The kit of claim 23, wherein said one or more DNA polymerases produce less than about 1% of amplification products containing one or more non-templated nucleotides at their 3′ termini.